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gb_p12:AF098962
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em_pat:E11286
em_pat:E11287
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gb_htg6:AC019785
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em_pat:E11292
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em_pat:E11291
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Database length: -486395729
Search time (sec): 887.180000
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Database: Gen
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Query: US-09-331-631-5_COPY_1_32
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gb_ba2:AF188287
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                                                                                                                                                                           gb_p12:ATAC013258
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уb_p12:AF161884
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                                            10 1 AC020260 Drosophila melanogas

10 1 AC018375 Homo sapiens clone R

13 1 AC013258 Arabidopsis thalian

14 1 AC008368 Homo sapiens chromo

15 1 AC005368 Homo sapiens BAC cl

17 1 AC005308 Homo sapiens BAC cl

17 1 AC00197 Homo sapiens chromo

18 1 AC001897 Homo sapiens chromo
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47 : ACC021467 Homo sapiens clone
93 : ACC019133 Homo sapiens clone
9 : AFC098962 Arabidopsis thaliana
1 : L47647 Homo sapiens creatine k
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9 i AC015623 Homo sapiens clone
i U04956 Streptococcus bovis amy
i U82323 pesulfovibrio vulgaris
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L04278 Xenopus laevis mRNA sec
! AC020788 Homo sapiens chromo
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X87619 B.taurus mRNA for thrombos
M87276 Mouse thrombospondin 1
X04665 Human mRNA for thrombos
AB005287 Bos taurus mRNA for t
         AF044393 Pleistophora
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gb_in2:AF044391
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Ratio: 5.625
Percent Similarity: 100.000
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TITLE
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TITLE
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17 nCysAspLysArgPheGluGluAspIleAspTrpSerLysTyrAsp
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US-09-331-631-5_COPY_1_32 x AF161885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macadamia integrifolia
Eukaryota; Viridiplantae; Strep
euphyllophytes; Spermatophyta;
Proteaceae; Macadamia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marcus,J.P., Goulter,K.C., Green,J.L. and Manners,J Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases i to 2141)
Marcus, J.P., Goulter, K.C., Green, J.L. and Manners, J.M.
A family of antimicrobial peptides is produced by proc
7.5 globulin protein in Macadamia integrifolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Plant Journal (1999) In press 2 (bases 1 to 2141)
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GRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNLERLHIAKFLQTISTPGQY
KEFFPAGGQNPEEPYLSTFSKEILEAALNYGTERLRGVLGQQREGVIIAKAGCGTRELT
RDDSBSRRWHIRRGGESSRGPYNLFNKRPLYSNKYGGAYEVKPEDYRQLQDMDVSVFI
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IEPQAMELAFAASRKEVEELFNSQDESIFFPGPRQHQQQSPRSTKQQQPLVSILDFVG
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/db_xref="taxon:60698"
/tissue_type="nut kernel"
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/product="vicilin precursor"
/protein_id="AAD54246.1"
/db_xref="GI:5852876"
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(AMP2) mRNA, partial
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AF044391 Glugea anomala sma
A83102 Sequence 13 from Pat
51
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alignment_block:
US-09-331-631-5_COPY_1_32 x AF161883
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AUTHORS
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LOCUS AF161883
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                                                                                                                                                                                                                     Quality: 180.00
Ratio: 5.625
Percent Similarity: 100.000
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                                                                                            Align seg 1/1 to: AF161883
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TITLE
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135 CAATGCATGCAGTTGGAGACATCAGGCCAGATGCGTCGGTGTGTGAGTCA 184
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                         GlnCysMetGlnLeuGluThrSerGlyGlnMetArgArgCysValSerGl 17
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Macadamia integrifolia vicilin precursor (AMP2) mRNA, AMP2-1
allele, complete cds.
AFI61883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-JUN-1999) Cooperative Research Center for Tropical Plant Pathology, The University of Queensland, John Hines Building, QLD 4072, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteaceae; Macadamia.

1 (bases 1 to 2182)
Marcus, J. P., Goulter, K. C., Green, J. L. and Manners, J. M.
A family of antimicrobial peptides is produced by processing
75 globulin protein in Macadamia integrifolia kernels
The Plant Journal (1999) In press
2 (bases 1 to 2182)
Marcus, J. P., Goulter, K. C., Green, J. L. and Manners, J. M.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
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                                                                                                                                                                                                                                                                                                                                                                                                 691
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QLETSGOMERCYSQCIKRFEEDIDWSKYDNQEDPQTECQCQRECRQESGPRQQQYC
QREKEJCEEEEEYNRQEDPQQYEQQOKHCQREETERHMQTCQQFCRCERYEKEKRK
QQKRYEEQQREDEEKYEERMKEEDNKRDPQQREYYEDCRRCEQQEPRQQHQCQLRCRE
QQRQHGRGGDMMNPQRGGSGRYEEGEEEEQSDNPYYFDERSLSTRFRTESCHISVLENF
YGRSKLLRALKNYRLVLLEANNNAFVLFTHLDANDYITLYIGGRGALKMIHHDNRESYN
LECGDVIRIPAGTTFYLLINDNNERLHIAKFLQTISTPGQYKEFFPAGGQNFEPYLST
FSKEILEAALNYQTEKLRGVFGQQREGYVIRASSGOIRELTRDDSESRHWHIRRGGES
SRGFYNLFUNKPRYSNKYGQAYEVKPEDYRQLOMDDLSVFIANVTQGSMMGPFFNTRS
SRGFYNLFUNKPRYSNKYGQAYEVKPEDYRQLOMDDLSVFIANVTQGSMGPFFNTRS
TKVVVVASGEADVEMACPHLSGCHGGRGGKRHEEEEDVHYDQVBARLSKREAIVVLA
GHPVVFVSSGNENLLLFAFGINAQNNEENFLAGRERNVLOOIEPQAMELAFAAPRKEV
                                                                                                                                                                                                                                                                                                                                                                                              EESFNSQDQSIFFPGPRQHQQQSPRSTKQQQPLVSILDFVGF"
508 c 571 g 412 t
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/protein_id="AAD54244.1"
/db_xref="GI:5852872"
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/db_xref="taxon:60698"
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Gaps:
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ORGANISM
                                          us-09-331-631-5
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                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                             BASE COUNT
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LOCUS AF161884
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Align seg 1/1 to: AF161884
                                                                                                             Percent Similarity:
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                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-JUN-1999) Cooperative Research Center for Tropical Plant Pathology, The University of Queensland, John Hines Building, QLD 4072, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marcus, J.P., Goulter, K.C., Green, J.L. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marcus, J.P., Goulter, K.C., Green, J.L. and Manners, J.M. A family of antimicrobial peptides is produced by processing of a 75 globulin protein in Macadamia integrifolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macadamia integrifolia.
Macadamia integrifolia
Macadamia integrifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Plant Journal (1999) In press 2 (bases 1 to 2182)
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1 (bases 1 to 2182)
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                                                                                                                                     Ratio:
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QQQQHGRGGDLINPQRGGSGRYEEGEEKSDNRYYEDERSLSTREGHISVLENF
YGRSKLLFALKNYRLVLLEANFUNAFYLPTHLDADAILLVTGGRGALKKHTERDKESYL
LECGDVIRIPAGTTFYLINRDNUERLHIAKFLQTISTPGQYKEFFPAGGONPEPYLST
FSKEILBALKTYQAERLRGVLGQQREGYIISAGQEJIRELTRODSESRRWHIRRGES
SRGPYNLFNKREPLYSNKYGQAYEVFEDYRQLQMDWSVFIANITOGGSMAWPFFNTS
TKYVVYVASGEADVEMACPHLSGRHGGRRGGKRHEEEEDVHYEQVKARLSKREAIVVPV
                                                                                                                                                                                                                                                                        GHPVVFVSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEV
EELFNSQDESIFFFGPRQHQQQSSRSTKQQQPLVSILDFVGF"
, 510 c 572 g 416 t
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QRRCKEICEEEEEYNRQRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Macadamia integrifolia"
/db_xref="taxon:60698"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="AMP2"
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                                             AF161884
from: 1
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                                                                                                             Gaps:
Percent Identity:
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GlnCysMetGlnLeuGluThrSerGlyGlnMetArgArgCysValSerGl 17

SOURCE

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JOURNAL
REFERENCE
AUTHORS
TITLE
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AUTHORS
TITLE
                                                                                                                                         alignment_block: US-09-331-631-5_COPY_1_32.x BTRNAT2
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ORIGIN
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KEYWORDS
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                                                                                                               Align seg 1/1 to:
                                                                                                                                                                                      Ratio:
Percent Similarity:
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1474 TAAACAGGATGGCGGCTGGAGCCACTGG
                                                       1424 TCCTCTGTGCAGACGCGGACCTGCCACATCCAGGAGTGTGACAAGAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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                                                                       7 ThrSerGlyGlnMetArgArgCys...ValSerGlnCysAspLysArgPh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-MAY-1995) R.S. Physiology, 540 E. Canfield, Location/Qualifiers
                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning and sequencing of bovine thrombospondin stimulatory effect of TGF-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BTRNAT2 2053
B.taurus mRNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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Zafar,R.S., Moll,Y.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombospondin; TSP-1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X87619.1 GI:860884
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                                                                                                               BTRNAT2
                                                                                                                                                                                      64.50
3.395
73.077
                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:Q28179"
/translation="MGLAWGLGVLLLLHACGS"
                                                                                                                                                                                                                                                                                                                                   /product="thrombospondin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="TSP-1"
180. .233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="aortic endothelium"
/clone_lib="lambda gt10"
/clone="pGEM-3Zf(-)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                          /gene="TSP-1"
/function="adhesive glycoprotein"
                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="TSP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="EcoI cloning site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moll, Y.D., Womack, J.F. and Walz, D.A.
                                                                                                                                                                                                                                                                                           625 c
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thrombospondin (partial)
                                                                                                                                                                                      Gaps: 1
Percent Identity: 46.154
                                                                                                              to: 2053
1501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
ACCESSION
VERSION
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ORGANISM
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                                         1457
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            22
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alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_ro:MUSTSPlA
                                                                                                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                             US-09-331-631-5_COPY_1_32 x MUSTSP1A
                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
1507 TAMACAGGATGGTGGCTGGAGTCACTGG 1534
                                                                                                                                          TCTTCGGTACAGACGAGGACCTGCCACATTCAGGAGTGTGACAAAAGATT 1506
                                                  eGluGluAspIleAspTrpSerLysTyr 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Characterization of mouse thrombospondin during cell growth and development J. Biol. Chem. 267 (5), 3274-3281 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (strain CD-1) embryo kidney cDNA to Mus musculus % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right) ^{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dixit, V.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4339)
Laherty,C.D., O'Rourke,K., Wolf,F.W., Katz,R., Seldin,M.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombospondin
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M87276
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GGGVQRRSRLCNNPTPOFGGKDCVGDVTENQVCNKQDCPIDGCLSNPCTAGAKCTSYP
DGSWKCGACPPGYSGNGIOCKDVDEGKEVEPDAG-FUHNGEHRCKNTDPGYWCLPCPPFT
TGSQPFGRGVEHAMANKQVCKPRNPCTDGTHDCNKNAKCNYLGHYSDPMYRCECKPGY
AGNGIICGEDTDLDGWPNENLYCVANATYHCKKDNCPMLPNSGDEDVDKGGIGDACDD
DDNDKIPDDROFFHYNPAQYDYDRDDVGGDRCDNCPKLPNSGDEDVDKGGIGDACDD
DDNDKIPDDROFFHYNPAQYDYDRDDVGDRCDNCPLEHNPDQADTBKNGEGDACA
VDIDGGGILNEEDNCQYVYNVDQRDTDMDGVGDQCDNCPLEHNPDQLDSSDSDLIGDTC
DNNOJIDEDGHQNNLDNCPYPNANQADHDKDGKGDACDHDDDNDGIPDDRDNCRLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OVRTIMHDPRHIGMKOPTAKMRISHRPKTGYIRVVMYEGKKIMADSGPIYDKTYAGG
RIGLIFVFSØBMVFFSDMKYECRDS<sup>R</sup>
1 1201 c 1144 g 885 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPDQKDSDGDGRGDACKDDFDHDNVPDIDDICPENFDISETDFRRFQMIPLDPKGTSQ
NDPNWVVRHQGKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDDYAGLVFGYQ
SSSRFYVVMMKQVTQSYWDTNPTRAQGYSGLSVKVVNSTTGPGEHLRNALWHTGNTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEDRACLYIDCDKMESAELDVPIQSIFTRDLASVARLRVAKGDVNDNFQGVLQNVRFV
FGTTPEDILRNKGCSSSTNVLTIDNNVNGSSPAIRTWYIGHKUQAICGLSCDE
LSSWYLELKCLRTIVTTLQDSIRKVTEENRELVSELKRPPLCFHNGVQXKNUREWFUD
SCTECHCQNSVTICKKVSCPIMPCSNATVPDGECCPRCWPSDSADDGWSPWSEWTSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MELLRGLGVLFLLHMCGSNRIPESGGDNGVFDIFELIGGARRGP
GRRLVKGQDLSSPAFRIENANLIPAVPDDKFQDLLDAVWADKGFIFLASLRQMKKTRG
TLLAVERKDNTGQIFSVVSNGKAGTLDLSLSLPGKQQVVSVEEALLATGQWKSITLFV
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3.395
73.077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="thrombospondin
/protein_id="AAA53063.1"
/db_xref="GI:567240"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="kidney"
212. .3724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="CD-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dev_stage="embryo"
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                                                                                                                                                                                                                          from: 1
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1
46.154
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AUTHORS
TITLE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawler, J. and Hynes, R.O.

The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth factor precursor. The third occurs as a continuous eightfold repeat of a 38-residue sequence; structural homology with parvalbumin and calmodulin indicates that these repeats constitute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           different proteins
J. Cell_Biol. 103 (5), 1635-1648 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87057617
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1 (bases 1 to 4434)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X04665.1 GI:37137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSTHROMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the multiple calcium-binding sites of thrombospondin. Data kindly reviewed (15-SEP-1987) by Lawler J.
                          /note="pot. N
2197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSSMYLELRGLRTIVTILODSIRKVTEENKELANELRRPPLCYHNGVQYRNNEEWTVD
SCTECHCONSVIICKVYSCPIMPCSNATYPDGECCPRCWPSDSADDGRSPWSEWTSCS
TSCGNGIOORGRSCDSLANRCEGSSVQTBTCHLOGENXERFKODGGWSHWSPWSSCSYT
CGDGVITRIRLCNSPSPOMNGKPCEGEARETKACKKDACPINGGWSHWSPWSCSVT
CGGCVQKRSRLCNNPTPQFGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGVKCTSYP
DGSWKCGACPPGYSGNAIQCTDVDECKEVPDACHNNGEHRCENTDPGYNCLPCPPRF
TGSQPFGQVGHATANKQVCKPRNPCTDGTHDCNKNAKCNYLGHYSDPMYRCECKPGP
TGSQPFGGGVEHATANKQVCKPRNPCTDGTHCNKNAKCNYLGHYSDPMYRCECKPGY
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DDDNKIPDDRDNCPFHYNPAQYDYDRDDVGDRCDNCPLEHNPDQADTDNNGEGDACA
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ADLDGDGIINERDNCQYYVNNDQRDTDMDGVGDQCDNCDLEHNPDQADTDNNGEGDACA
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DNNQDIDEDGHONLDNCPYUPNANQADHDKDGKGDACDHDDNDGIPDDKNRCRLYP
                                                                                                                                                                                                                              /product="mature 817. .825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA28370.1"
/db_xref="GI:37138"
/db_xref="GI:37138"
/db_xref="SWISS-PROT:807996"
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/translation="MGLAWGLGVLFLMHVCGTNRIPESGGDNSVFDIFELTGAARKGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPDQKDSDGDGRGDACKDDFDHDSVPDIDDICPENVDISETDFRRFQMIPLDPKGTSQ
NDPNMVVRHQGKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDDYAGFVFGYQ
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                                                                                              /note="pot. N-glycosylation site"
1636. .1644
                                                                                                                                                                                                                                                                                                                                                                                                                          QVRTLWHDPRHIGWKDFTAYRWRLSHRPKTGFIRVVMYEGKKIMADSGPIYDKTYAGG
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QEDRAQLYIDCEKMENAELDVPIQSVFTRDLASIARLRIAKGGVNDNFQGVLQNVRFV
FGTTPEDILRNKGCSSSTSVLLTLDNNVVNGSSPAIRTNYIGHKTKDLQAICGISCDE
                                                                                                                                                                 /note="pot. N-glycosylation site"
1153. .1161
                                                                                                                                                                                                                                                                                              /product="put. signal peptide (AA -18
130. .3585
                                                                                                                                                                                                                                                                                                                                                                                            RLGLFVFSQEMVFFSDLKYECRDP"
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/db_xref="taxon:9606"
/cell_type="umbilical vein endothelial cells"
'note≖"pot. N-glycosylation site"
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                                                                                                                              CDS
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                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (30-JUN-1997) to the DDBJ/EMBL/GenBank databases.
Akemichi Ueno, TheyUniversity of Tokushima, Department of
Biochemistry, School of Dentistry; Kuramoto-cho 3-18-15, Tokus
Tokushima 770, Japan (E-mail:akemichi@dent.tokushima-u.ac.jp,
Tel:+81-886-33-7326, Fax:+81-886-31-4215)
On Apr 21, 1999 this sequence version replaced gi:2244706.
Location/Obalifiers
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CDNA cloning of bovine thrombospondin 1 and its odontoblasts and predentin

Biochim. Biophys. Acta 1382 (1), 17-22 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (strain:Holstein) two weeks after birth male anterior tooth odontoblast cDNA to mRNA, clone:pBTS1-28.
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thrombospondin 1.
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
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                                     /product="thrombospondin 1"
/protein_id="BAA21115 1"
/db_xref="GI:2244707"
                                                                                                                                                                                                       /db_xref="taxon:9913"
/cell_type="odontoblast"
/clone="pBTS1-28"
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/3274. 3282
/note-"pot. N-glycosylation site"
1 1185 c 1177 g 933 t
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/translation="MGLAWGLGVLLLLHACGSNRIPESGGDNSVFDIFELTGAARKRS
GRRLVKGPDPSSPAFRIEDANLIPPVPDKKFQDLVDAVRAEKGFLLLASLRQMKKTRG
                                                                                                                                                                  /dev_stage="two weeks after birth"
/sex="male"
                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/strain="Holstein"
                                                                                                  /codon_start=1
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                                                                                                                                              type="anterior tooth"
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seq_name: gb_pr2:HSTS
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Quality:
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2083. .2
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73.077
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2671. .2784
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1789. ..
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VTCGNOJQQGRSCDSLNNRCESCSVQTRTCHIQECDKRFKQDGWSFWSFWSCSVT
CGDGVITRIRLCNSPSPQMNGKPCEGKARETKAQQKDSCPINGGWSFWSPWSCCSVT
CGDGVITRIRLCNSPSPQMNGKPCEGKARETKAQQKDSCPINGGWSFWSPWDICSVTC
GGGVQKRSRLCNNPKPQFGGKDCCVGDVTENQICNKQDCPIDGCLSNPCFAGVQCTSYP
DGSWKCGACPPGYSGDGVECKDVDECKEVPDACFNNAECNYLGHYSDBWYRCECKPGPPRF
TGSQPFGRGVEHATANKQVCKPRNPCTDGTHDCNKNAECNYLGHYSDBWYRCECKPGY
AGNGIICGEDTDLDGWPNEDLLCVANATYHCRKDNCPVLHQPDQADTDNNGEGDACD
DDDNDKIFDDRDNCPHYNPAQYDYDRDDGDGDDCDNCPLENPDQADTDNNGEGDACA
ADIDGDSILNERDNCQYVNVDQKDTDMDGVGDQCDNCPLENPDQADTDNNGEGDACA
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DNNQDIDEGGHNNLDNCPYVPNANQADHDKDGKGDACDHDDNDGIFDDRDNKCRLVP
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2893. .3000
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1627. .
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SSSRFYVVMWKQVTQSYWDTNPTRAQGYSGLSVKVVNSTTGPGEHLRNALWHTGNTSG
QVRTLWHDPRHIGWKDFTAYRWHLSHRPKTGFIRVVMYEGKKIMADSGPIYDKTYAGG
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QEDRAQLYIDCEKMENAELDVPIQSIFTRDLASIARLRIAKGGVNDNFQGVLQNVRFV
FGTTPEDILRNKGCSSSTSVFVTLDNNVVNGSSPAIRTDYIGHKTKDLQAICGISCDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hennessy,S.W., Frazier,B.A., Kim,D.D., Deckwerth,T.L. Baumgartel,D.M., Rotwein,P. and Frazier,W.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human mRNA for thrombospondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89139590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calcium binding protein; glycoprotein; thrombospondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X14787.1 GI:37464
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                                                                                    Ratio:
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                                                                                                                                                                                                         ρ
                                                                                                                                                                                                                                                                                                                                                                                                         SCTECHCQNSVTICKKVSCPIMPCSNATVPDGECCPRCWPSDSADDGWSPWSEWTSCS
TSCGNGIQQRGRSCDSLNNRCEGSSYOTRTCHIQECDKRFKQDGGWSHWSPWSSCSVT
CGDGVITRIFLCNSPSPDMFCPCEGEARETKACKKDAFG
GGGVQKRSRLCNNPAPQFGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGVKCTSYP
DGSWKCGACPPGYSGNGIQCTDVDECKEVPDACFNHNGEHRCENTDPGYNCLPCPPRF
TGSQPFGQGVEHATANKQVCKERNPCTDGTHDCNKNAKCNYLGHYSDDMYRCECKPGY
                                                                                                                                                                                                                                                                                         5697.
                                                                                                                                                                                                                                                                                                                             /product="thrombospondin (AA 1 to 1139)"
5518. .5559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRRLVKGPDPSSPAFRIEDANLIPPVPDDKFQDLVDAVRAEKGFLLLASLROMKKTRG
TLLALERKDHSGQVFSVVSNGKAGTLDLSLTVQGKQHVVSVEEALLATGQWKSITLFV
QEDRAQLYIDCEKMENAELDVPIQSVFTRDLASIARLRIAKGGVNDNFQGVLQNVRFV
                                                             64.50
3.395
73.077
                                                                                                                                                                                                     /note="polyA site"
1388 c 1387 g
                                                                                                                                                                                                                                                 /note="polyA signal"
5722
                                                                                                                                                                                                                                                                                                                                                                                        RLGLFVFSQEMVFFSDLKYECRDP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGTTPEDILRNKGCSSSTSVLLTLDNNVVNGSSPAIRTNYIGHKTKDLQAICGISCDE
LSSMVLELRGLRTIVTTLQDSIRKVTEENKELANELRRPPLCYHNGVQYRNNEEWTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="precursor polypeptide (AA -31 to 1139)"
/protein_id="CAA32889.1"
/db_xref="GI:37465"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="fibroblast and epithelial"
/clone_lib="lambda gtl1 and pUC19"
/clone="6A,S10,TXE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                            /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT:P07996"
/translation="MGLAWGLGVLFLMHVCGTNRIPESGGDNSVFDIFELTGAARKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="signal peptide (AA -31 to -1)"
|12. .3629
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.5702
                                                               Percent Identity:
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SOURCE
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                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                                                                                                       ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: XELSTAGE from: 1 to:
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                                                           AUTHORS
                                                                                                                                  ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                     1255 TCCTCTGTACAGACACGTTCTTGCCAAATCCAGGATTGTGACAAGAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1357 TCCTCGGTCCAGACACGGACCTGCCACATTCAGGAGTGTGACAAAAGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAACAGGATGGTGGCTGGAGCCACTGG 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eGluGluAspIleAspTrpSerLysTyr 31
                                                                                                                                                                                                                                                                                                                gb_htg14:AC020788
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Ratio:
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1 (bases 1 to 197071)
Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Budota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C. David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XELSTAGE 3522 bp mRNA
Xenopus laevis mRNA sequence
L04278
                                                                                                                                                                                                                      Homo sapiens chromosome 3 cl
PROGRESS ***, 113 unordered
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                Homo sapiens
                                                                                                                                                                  HTG; HTGS_PHASE1.
                                                                                                                                                                                     AC020788.2 GI:7007946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L04278.1 GI:295541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
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3.289
73.077
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786 c 884 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Xenopus laevis"
/db_xref="taxon:8355"
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                    Cox, C.,
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-JAN-9000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Feb 19, 2000 this sequence version replaced g1:6886414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It current consists of 113 contigs. The true order of the pieces is not known and their order in this sequence record
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.980611
Consensus quality: 103326 bases at least Q40
Consensus quality: 135876 bases at least Q30
Consensus quality: 151983 bases at least Q20
Estimated insert size: 165698; sum-of-contigs estimation
Quality coverage: 1.2x in Q20 bases; sum-of-contigs estimation
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15459 15479 9670 9690 10485 10505 11292 11292 11312 12094 13122 13122 13124

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g of 1216 bp in length
f unknown length
g of 813 bp in length
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g of 1133 bp in length
f unknown length
g of 794 bp in length
                                                                                                                                                                                                                                                                                                                                                                  f unknown length
g of 1246 bp in length
f unknown length
g of 827 bp in length
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g of 1096 bp in length
f unknown length
g of 1148 bp in length
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g of 1121 bp in length
f unknown length
g of 788 bp in length
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f unknown length
g of 1102 bp in length
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g of 1195 bp in length
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g of 864 bp in length
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of 795 bp
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of 860 bp in length
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of 685 bp in
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of 1159 bp in length
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of 782 bp in
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of 787 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-331-631-5_COPY_1_32 x AC020788/rev
                                                    REFERENCE
                                                                                                                                                                                                                                                                                                     seq_name: gb_ba2:AF188287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS AF188287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                   30610 ATGTGACAGGTCATGGAGGTCTGAACTGAAGTGGTGCTCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnCysMetGlnLeuGluThrSerGlyGlnMetArgArgCysValSerGl
                                             Stigmatella aurantiaca
Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystgbacterineae; Cystobacteraceae; Stigmatella.
1 (bases 1 to 42603)
                                                                                                                                                                                                Stigmatella aurantiaca
AF188287
                            Silakowski, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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                                                                                                                                                                            AF188287.1 GI:6635393
        Nordsiek,G., Brandt,P.,
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                              Schairer, H.U.,
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Gaps: 1
Percent Identity: 41.935
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gap of
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        Bloecker, H.,
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J of 1218 bp ...

Jf unknown length

ig of 1632 bp in length

mknown length

n in length
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of 1783
unknown
of 1560
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of 1441
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of 1255
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of 1302
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of 1016
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of 1202
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of 1310
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of 1368
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of 1218
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of 1153
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of 1064 bp in length
unknown length
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of 1738 bp in length
unknown length
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of 1051 bp in length
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of 754 bp in
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of 855 bp in length
                          Ehret, H.,
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      H., Kunze,B., Weinig,S., Hoefle,G., Beyer,S. and
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New lesson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New lessons for combinatorial biosynthesis from myxobacteria. T myxothiazol biosynthetic gene cluster of Stigmatella aurantiaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Braunschweig 38124, Germany
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Nordsiek,G., Brandt,P., Bloecker,H., Hoefle,G., Beyer,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 274 (52), 37391-37399 (1999)
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                                                                                                                                                                                                               ACSSSLVAIHEACRSLRSGESSLALAGGVQLNLSPRTFMAVSAFGALAPDGRCRTFDA
RASGYVRGEGGGVLVLKPLSRALADGDAIYCLI RESAVUNDGASNGLTAPNPKAQERL
LRDAY AVAGMDPAQVHYVELHGTGTPLGDP IEAGALGAVLGAAREAERPLHVGSVKTN
IGHLEAAAGIASVI KVALSI RHQQLPASLHFEQPNPRI PFDDLRLRVQTOLAPWPAEK
DPAVAGI SAFGFGGTNCHVVVEEHRGGSRTAAVPVSTPHAQSPRHPKTAFLFAGAGSA
WMGMGRELLGAEPVFRAFEECCDAAF PLGGWSLVPALLAPRVSRSFEDGEEQLPLVL
AFOISLAALNRSWGIEPSATVCYSVGEWAAAQVAGILTI EEVFALAXHYLTQVQKGVAG
GVGMAVVGLSGAEVAERIAPYGGRIS I ASENGPRSTGLGGEAAALQDFTASMTAAGI F
ARLVELDFYAHI POVEALKPLFLQSCPVLRPSGPRSVMENTVSGAFVDGGTLGAEXWA
SNFREPVRFATAMRTLLEGGYDVVLDVWHPPIHEBSVLENVRAGTASAEFIASMERGE
PSVEGLHRALTQLSQAGGPVRWERVVPGTGAGSSAPVRTELFVASARTEQALREQALREQALR
IAEQLERDAASSLTDLCYTAGARRSHEHRLALVAETRALEEGLAAFAGGEIRPNPS
GAGGERRAASSLTDLCYTAGARRSHEHRLALVAETRALEEGLAAFAGGEIRPNPS
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                                                           LSLEEALSLVVSRSRLMGRAAGQGGMATVEASPARIEPLLGKCGTDLAIAAVNGPENV
VVSGALAALASLRDELTGQGLRVRVLNVNYAFHSAQMAPYLGDLDPVLRELKPKPPRL
PIYSTVHGRLASASDFGTDHWRANVRERVLFAPAVEAMRADGHGAFVEISPHPVLLQP
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/note="PKS; MtaB loading domain and module 1: polyketide
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module 2: polyketide synthase domains: KS, AT, DH, KR,
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ALHAERESQHPPRTEIEQPLLFAFQVALAALMESWGIRPDAVVGHSVGEISAAHVAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSRTGVFTGMVWRDYADLQTIHNAAPTLHTCTGYAGGIIANRISYALGLEGPSLAIDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPTSSPALPLIKLPPDEVHYMIVEPERITEPGLLESYRALLDPG
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QRERFFDYMTLKEAYIKARGMGLSLPLDQFAFEVSQGLSTRISFDPRLVDEPSQMQFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (20-SEP-1999) NBI/MX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAF19810.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="MtaA"
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GASEARANDER REFERMALS KREASKERS VIGARIVGAST KELKKRLESLIG VURATIV
GELPESAR PIDERREFLOEGGISSIMALOF RINSLAAS GERSIPATILI DEBETTEKKLEFET
ARDLITERSERAP IDERREFLOEGGISSIMALOF RINSLAS GERSIPATILI DEBETTEKKLEFET
GELPESAR PERARS REPKELERA I AVDAGAGET I AVVGMACTENGSYRS PEEFWRLLANG
VNAVREVEKDRWSZIDTWYD DDETPGKWYSTHGETGLESDYRLLENSPDPTGINAYSG
SOGVLSVAAGRI AYALGLEGPTIA VDTACSSSLVAAHLACOSLRNGECDLALVGGSNL
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RSLVGGLF I AGVT PAWNRLF PEGGSLVSLPS YPWOKERYM I AS PTSARLQLPAPSOGV
LHGRRVKSPLABST FETTOLS VEKMPFLERHLHGALVVAAGAHVALASALRELAGAD
VERLAPUTLARGEN STORTERACH PEGGSS LVSLPS YPWOKERYM I AS PTSARLQLPAPSOGV
LHGRRVKARPSAROUTHERE LESSAR TLAGAPSOGVER PREAPGREEAPT LARGEWYL
PASGVEGERACH LARGE PROBLEVS PYYKAMDAEGIC LARREQVCHVLAAPESA
VTGEALLFORWESANDERS PEDALAAA PURDABETLACT LIDLDPDP
AADGVGCLFQELLT PDREDLIAMRGGARFAQRLS FLEAVPEPGTAP I SPDGTYLLTGG
LGGIGLRCARWLVDAAARAFULDEDDF PROBLEWS PLAGAL BOOGNES FERAR DETOFLILE BATGEFERAT LARGEBACH LERGT VROAT BEBLA
VELAGTIS SI PAMLGGEGGGY SAANAFLDALAFARRAGGLFAN SCAVIGHLANG PWARVEGHA
VARASERSAHLAALGIES I PDEGVSAARAFULRAASAHVGIF OLDWITTROORHAEGHA
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gene

CDS

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DLEHTHESGVEVMRQRAQMKKGNGAIMPVFTSLLGHRSRVPGGGSPFSWLGEVVYAI TQTPQMMLDHQVREËAGÄLYCHWDSPEGLFPEGLLEGAFEAYTDLLSRLADDNALMEE GTVVRLPEAGYARRETTNATTASI PEARLDGLFLAQAEOGPQPKMAILEPALRMSYGEL LGQAGSLAAHLAELGARPNELTAVVLEKGWRGJVAVTAIHLAGSAYLPTDPALPEERR RLLLEEGQVKVVLTESHLAERLSWPASVRVVAIADTARGAPPRLPARAASDMAYCIYT /note-"peptide synthetase; peptide synthetase domains: Heterocyclisation, adenylation, PCP note: motif with weak homology to putative NAD binding proteins from Pyrococcus species located behind PCP; this motif may be involved in-thiazole formation from the proposed thiazoline intermediate of the biosynthesis of myxothiazol" SGSTGRPKGVKIEHRAAANTILDINERFGVGPADRVFALSSLGFDLSVYDIFGSLAAG AAIVLPQPEVjjrdPAHWLQVLRQQGVTIWNSVPTLMEMLVDQVEARGELLPETLRLVM /product="MtaC" transl_table=11 'codon_start=1

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AF188287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-331-631-5_COPY_1_32 x AF188287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                              29166 CTTCCGGGCCCATGTGGACTGGTCT 29190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29116 CTCCGGACCTCGCCGGTGTTCCGCAAGGCACTCGAGGAATGCGACCAGGC 29165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LeuGluThrSerGlyGlnMetArgArgCysValSerGlnCysAspLysAr 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gPheGluGluAspIleAspTrpSer 29
                                                                                                                                                                                               AC019039 162168 bp
Homo sapiens chromosome
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                    HTG; HTGS_PHASEO
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                   AC019039.2 GI:6922690
                                                                          human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEQLLEHLRSASRSANLOTVASPPDAASRFAPFPLTDIQNAYWVGRQGAFDAGGVAAH
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STELLERGACVNTLLDHRGAVNTLLDMNERENVGPEDRVLALSSSLSFDLSVDLEGVLAAG
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3.100
80.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLQPSRASGLTDARGGKILSAIMRLVSEVLKRPSIEPEAGLLQLGATSVELIKLSMML
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AFSLLLVGDRRVISQRYGERWRDLALIEAGLMAQLLETRAAESDLGLCQLEELRFEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGGDWIPVTLPDRIRRLSRDIRVISLGGATEASIWSIIHPIGRVDPAARSIPYGRPML
NQREYVLDEKLAPRPHYVFGDLYIGGVGLAQGYFRDEETTRAFERHPRYGERLYRTG
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LVAYLVPVEGQEAPSDEVLRSFLAAALPQYMVPAVFVRLEHLPLSSNGKVDRKALPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {	t GAIVMPEPGTSRDPGRWQVLLEKTGVTIWNSVPALMDMLVEFSEGSGLRLPDSLRLVL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"MtaD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MtaC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 40.000
                                                                                                                                                                                                                                 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 42603
                                                                                                                                                                                                                          A HTG 06-FEB-2000. clone RP11-390D24 map 18, LOW-PASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
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REFERENCE
AUTHORS
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AUTHORS
TITLE
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alignment_block:

SOURCE

ORGANISM

KEYWORDS VERSION

ACCESSION DEFINITION

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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreita, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Landers, T., Lehoczky, J., Levine, R., McGurk, A., McKernan, K., McChandla, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
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Direct Submission
Submitted (30-DEC-1999) Whitehead Institute/MIT Center for Genome Submitted (30-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 7, 2000 this sequence version replaced gi:6648222.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria; Primates; Catarrhini; Hominidae; Hon
1 (bases 1 to 162168)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This record contains 175 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pdss sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved.
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Center clone name: 390_D_24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
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US-09-331-631-5_COPY_1_32 x AC019039/rev
                                                                                     seq_name: gb_pr4:AC011331
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REFERENCE
AUTHORS
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ORGANISM
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LOCUS CELC48E7
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US-09-331-631-5_COPY_1_32 x AC011331/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: AC011331 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54612 TGAAATGGCCATGGCCACGTGACTTGCTTTGGCCAGTAAAATATGAG 54567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sAspLysArgPheGluGluAspIleAspTrpSer...LysTyrAsp 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCATATCTCTCCTCCTCTGGGCAATGGTAAAAATGTACTTCCCAATC
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J., Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favel, Fulton,L., Gardner,A., Green,P., Hawkins,T., Hilier,L., Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N., Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (06-OCT-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA At location 59145 there is a subclone variation in which one subclone calls a 'G' and all the rest call 'A'. From 94100-94174 there is single-strand/single chemistry. At 148425 there is a subclone variation in which one subclone calls 'T' and all others
                                                                                                                                                                                       Caenorhabditis elegans strain-Bristol N2.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea;
Rhabditina; Rhabditoidea; Rhabditidae; Pelc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spiegel,L.A., Preston,R.R., Matero,A., Snan
Rodriguez,M., Shekhar,M., Schutz,K., See,L.
Habermann,K., Dedhia,N.N. and McCombie,R.W.
                                                                                                                                           1 (bases 1 to 37701)
Wilson, R., Ainscough, R.,
                                                                                                                                                                                                                                                                                                                                          AF000262
                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans cosmid C48E7.
                                                                                                                                                                                                                                                                                                                    AF000262.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang, E.N., Nascimento, L.U., de la Bastide, M., Vil, D., Spiegel, Preston, R., Matero, A., Shah, R., O'Shaughnessy, A., Rodriguez, M., Shekher, M., Schutz, K., See, L.H., Swaby, I., Habermann, K., Dedhia, N.N. and McCombie, R.W.
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic Sequence for Homo sapiens clone H_NH0514011, Chromosome 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 175278)

1 (bases 1 to 175278)
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2.674
71.875
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36801 c 37956 g
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                                                                                                                                                                                                                                                                                                                    GI:1947126
                                                                                                                                                                                                                                                                                                                                                                                         37701 bp
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Percent Identity:
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                           McMurray, A., Mortimore, B.,
                                                                                                                                                                                               Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                       ANI
                                                                                                                                                                                                                     Rhabditia; Rhabditida;
                                               Laister, N.,
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                                                                                                                                             Berks, M.,
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                                                                                              Favello, A.,
                                                                                                                                                                                          Caenorhabditis.
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                                                                          Jier, M.,
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JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
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AUTHORS
                                                                                                                                     COMMENT
                                                                                                                                                    TITLE
JOURNAL
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                                                                                                                                Submitted (18-APR-1997) Submitted by:
                                                                                                                                                                                                                                      The sequence of C. pelegans cosmid C48E7 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                             94150718
                                                                                                                                                                                                                                                                                                                                                                                  Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                            Direct Submission
                                                                                                                                                                                              Waterston, R.
                                                                                                                                                                                                                                                                                  Wamsley, P. and
                                                                                                                                                                                                                                                                                                                                                Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                       elegans
                                                                                                                                                                                                                    (bases 1 to 37701)
                                                                                                                                                                                                                                                                                                      (bases 1 to 37701)
St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                              Genome Sequencing Center
Department of Genetics,
St. Louis, MO 63110, US
                                                                                                                                                                                                                                                                                  Kramer, J.
                                                                                        Washington
                                                                                        University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roopra, A.,
Sonnhammer, E.,
                                                                                                                                                                                                                                                                                                                                                                                           G
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NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

The 5' cosmid is T08B2, 700 bp overlap;3' cosmid is C10G11, 700 bp overlap. Actual start of this cosmid is at base position 1 of CELC48E7; actual end is at 6598 of CELC10G11

NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation)
Location/Qualifiers

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FEATURES
                                                                                       CDS
                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                           /gene="C48E7.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ∕organism="Caenorhabditis elegans"
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       .7829,
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. .10611,
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19162

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GIVYYKAFSTEEEVHEIVQLEVRADNVQPARTTLPTTILRADMENYDDFSTTGDOMIPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNFTQQDIDEGAIŠYKLHYQQYSIVNDFFVFRVVSPAVSSPLLRFDIVYVPŘESSIRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNGGSDSTKFSIFGENNLPVVILGAIVAATIFVLICRRCGEGKKKNKTRTPINAKLDT
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RRQNVSSLDYAGITSDTPPPMRLFEQVAQTQPTNHYWV"
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                                                                                                                                                                                                                                                                                                                                                                              olfactomedin (SP:Q07081)"
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FVLNGTETMSISRQNLFSWTFPKSFSAHNLIYHIDEPPKLGTLSRKLAVGKQRRIGVS
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KVNEFSHKQLIEELVSLVDEGTELGSGRIRLIARDREARSGVVILETQSTKVDVKLVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="the second exon has similarity to collagen alpha
a glycine- and proline-rich region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(15632. .15766,16026. .16439,16596. .16877)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITFRSKAYFQILSNYSEVEGCVKICLKNYTLDEEIEETITTPVAYIQGVTARKYYIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAB52938.1"
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                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                 'note="last two exons have similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                 part of
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                                                                                                                                                                                                                                                             ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name:
                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block: LOCUS AC003033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-331-631-5_COPY_1_32 x CELC48E7/rev
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                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36526 AAAGCTGAAGCAAAATGTCGAGTTTCTGTATTAT 36493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36576 AAATTCGAAACTAGGGGTAACCCGCAAAGATGTGCGACAATGTGCGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 sArgPheGluGluAspIleAspTrpSerLysTyr 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnLeuGluThrSerGlyGlnMetArgArgCysValSerGlnCysAspLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_pl2:AC003033
                                                                  Etkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                 HTG
                                                                                                                                                                                                                                                                                            complete sequence.
AC003033 AE002093
AC003033.2 GI:6598385
                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                      thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
(bases 1 to 84254)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WIRENGYLROELI IDYLIGGGSKGYMYNLNVKKEETIEDPOGDRTQY ITQNNAHLME KINETRAKPMSMESITASLITDLQRLVKENGLULAKPD IELAGQILVDESDGIIRKIGE SNGGIETUDIRRAIROICCHHCCSLIREOFECRAIRVMRLLENRHYLDEEQVEKLSMM SGKEAREMLYALVEEGYVFNKPVGRSNDFQFARTFYLLYYDLPRTIRGLVEYTCKLVR NLIVROHEETENKSVLDKDANVQPIIENIRSSEQLDEASKLAQIAEVBEMYLPGPDR AQLNERKKAQATLAAQDQSIRVLLSEKLFLASGEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence-not_experimental
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TEQEAFADLVAELETQTAEAVKAFSKVFDRMEETNDDKEGLSLLKLKKYEMTAYLGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.00
2.542
85.714
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GPAAESICVELISQGRLTYSETIRRIQATDETAVFSDIKKSFEELAAAHFLIRVPSYE
SEIHGCPQFYTNFDPFAISTNIMEKKEGTSTSDSTSNNRKRKADSTPEDGDAGQYWRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"region of weak similarity to a short region of DNA-directed RNA polymerase III, 74 kd subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Join(20378. .20440,20486. .20578,20641. .20762,20811. .2
21566. .21885,21945. .22089,22152. .22363,22461. .22856)
/gene="C48E7.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSSKGNHÄVRLDNMDVEGDEEEEEEEDEDDEEGKGAKEVKKYVAPRIRAVRYEEEDEAP
NKQQEKAKRRAMQSSLIMELKNQYSDAPEEIREMSEKKYQYDRERERYEEDNFTRIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence-not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVLMSKMMKGESITVEPSVKRALKHRVFIEKMKPVEDKMKPQIEKLLGRSSAESGASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(18420. .18517,18563. .18650,18698. .18808,19037. .1
19210. .19347,19393. .19642,19687. .20002,20050. .20176)
/gene="C48E7.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSQKERKKAAKGKKEGRKRAIRRRQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    84254 bp
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Gaps: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                   mRNA
                                                                                                                                   gene
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/gENGCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, first Carlos Control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-DEC-1999) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:2702261. The sequence and annotation of chromosome 2 were merged from thos of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Address all correspondence to:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prediction programs including GRAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 database support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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20083487
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                                                                                                                                                                                                                                   /rpt_family="(GAA)n"
<331. .>1332
                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1.
                    /gene="At2g32820"
/note="F24L7.4; predicted by genefinder and
                                                                                                                                   /gene="At2g32820"
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/chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                            Sequence from
                                                                                                                                                                                                                                                                                                                                                                            clone F24L7"
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                              genscan"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="T21L14.22; predicted by genefinder" complement()oin(7648. .7741,7838. .7917,8011. .8118, 8228. .8305,8403. .8442,8533. .8585,8715. .8747,8829. .9383)) /gene="At2g32840" /note="hypothetical protein"
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11802..11967,12058..12524))
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PQPQTPASSYRALAPLHRHHPHQNIYINPLPIRSROYVTNSPHQPPHPDPSSLIYPFG
SSGRGFPTRPVRQNSNSVADPVGSPSPGGYTPRGPVKGYHHGQFVSNLDPMNQFMRAA
HPQNQOSPQLGSGHMKGVPHFLQPRLVLVSENVYVEATPSPTSLLDNSCHKKARSRDD
ALVLVRKRKYRITEGASLYSLCRSWLRNGAHEGIKRIDMMTCLPKPLPVDKTETSLPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="(TAAA)n"
complement(join(<7648 . .7741,7838 . .7917,8011 . .8118,
8228 . .8305,8403 . .8442,8533 . .8585,8715 . .8747,8829 . .>9383))
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EALLAMDFCGKSLYDVLENRGAGYFEEKQALTIFRDVCNAVFAMHCOSPRIAHRDLKA
ENLLLSSDGQWKLCDFGSVSTNHKIFERAEEMGIEEDNIRKYTTPTYRAPEMWDLFRR
                                                             /translation="MWKfKpFAQKEPAGLEGRFLEIGNLKVQVRNVIAEGGFSSVYLA
QDVNHASKQYALKHMICNDEESLELVMKEISVLKSLKGHPNVVTLYAHGILDMGRNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(9789. .11142,11327.
11802. .11967,12058. .>12524))
/gene="At1932850"
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GKSLEEISREDEEQSGGDTVVEMTVANSGRKVPV"
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TMNAIHEVFTVSKAQTLIALCGTVPGYWFTVAFIDILGRFFIQLMGFIFMTIFMFALA
IPYDHWRHRENRIGFLIMYSLTMFFANFGPNATTFVVPAEIFPARLRSTCHGISAASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAKKGKEVLNALDAAKTQMYHFTAIVIAGMGFFTDAYDLFSISL
VTKLLGRIYYHVDSSKKPGTLPPNVAAAVNGVAFCGTLAGQLFFGWLGDKLGRKKVYG
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RGAFTAAVFAMGGFGILAGGIVSLTVSSTFDHAFKAFTYEVDFVGSTVPQADYVWRIV
LMFGAIPALLTYYWRMKMPETARYTALVARNTKQAASDMSKVLQVDLIAEEEAQSNSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(2300. .3151,3250. .3722,3900. .4203))
/gene="At2g32830"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(<2300. .>4203)
/gene="At2g32830"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(<2300. .3151,3250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1231. .81848)
/note="Sequence from clone T21L14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MYMKIAIATERTDLPRLYSTAIRASNSQNASDVERCEDVLRYLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLPPFGEQCRNE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLVEEAICEEDKEDEESVKHLSESDLLKRHIDRAKKVRARLREERLKRIARYKARLAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative phosphate transporter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="T21L14.23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="At2g32830"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDILALLMKFSIISTAIETRRIMEKLERLTKHKDRKICNAALALLHHWRQTIRNQQQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLNMKKHQPVKAFENPKTCLVLKKNSPEMLELFEMAKKSADVANAKGFLAAKEEASIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAB91965.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="At2g32820"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5600
                                                                                                                                                                                                                                                                                                                        .11142,11327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3722,3900. .>4203))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .11576,11666. .11716,
                                                                                                                                                                                                                                                                                                                            .11576,11666. .11716,
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gene

mRNA

CDS

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alignment_scores:
Quality:
Ratio:
Percent Similarity:
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US-09-331-631-5_COPY_1_32 x AC003033
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                                                                                                                                  9237 TGTTTGAGGTTGAGGTTGAGACGACGGCGTTATGACTGTGTTAGGTTGTG 9286
9287 TCACCGGAGATTCAGATGCGGTGACGATTGGAGTCGATAC 9326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                sAspLysArgPheGluGluAspIleAspTrpSerLysTyr 31
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LAKELNINGFRESISHTRILPYGTIKKVENEGKYENDLINELLANGIQPSVTLFHW
ESPLALEMEYGGFLNERIVEDPREFANNCFKEFGDRVKWWATFNEPSVYSVAGYSKGK
KAPGRCSKWQAPKCPTGDSSEEPYIVAHNQILAHLAAVDEFRNCKKVEGGGKIGIVLV
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GIVIYPAGLKNILKHIKDEYMDEIYIMENGMDEIDYGTKNITEATNDYGKKEFIKSH
ILMGKSIRMDKVRLKGYYINSLMDNFEWDKCYKVRFGLYYDDYNDNMKRYIRSSGKW
ICETIOENGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSEFLDSKETLHKCYFEGHREKGYAPKLFDVEYLEPENSQLSYRSDFM"

complement(18507. 19090)

/note="molecular marker g6191"

complement(join(19158. 19966,20113. 20413,20521. 20672,
20766. 20895,20993. 21068))

/gene="Atg32870"

complement(19158. 21068)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.00
3.389
60.000
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LQASPDERPDITQVKSQFLLIVSSQLKKCKMSITTCSSKSATKPSPAPRRSPPPPPS
SGESDSGGPLGAFWATOHAKTSVVSEDNKNMSFDERNSTTSKSERVEVDSHQPKKPS
PVRGEARGIQRNKDLETTISQKNTTPAAANNMTRVSKDDAFNSFVADFDTTKFDNGNK
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PGKEEALEASIQRKDELKOTKSEKABITAKEFKLSAICRSQROELQDLKQTLASKSA
SPSPSRDSSQNQPSPGMHSMSSTPSVLFLVLLFLSLDTHTKVFINVYLTILMFLMKQR
DKMEGTMWELQDQRSNWSTGSSDTNSWQPFSDEAKPVMESAASKGNNNTINQSVWSTRSK
PKASAAGTQGEEPWGFETESFRAAATSAAATSASGTQRSMGSGNSTSQRYGNSKMRENQ
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/oin(14780. .15518,15202. .15271,15365. .15423,15533. .15608,
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16793. .17010,17342. .17479,17581. .17689,17849. .18143)
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Gaps: 0
Percent Identity: 36.667
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mRNA

gene